

CLASS A GROUP II							
A1AB_human	α_{1B} -adrenergic alpha 1B-AR		TMDI junction between TMDIII and IC2		63 FAIVGNILVIL A 142 CAISIDRYIGV A	IP / COS-7	(Scheer, Fanelli et al. 1997)
A1AB_human	α_{1B} -adrenergic alpha 1B-AR		junction between TMDIII and IC2		143 CAISIDRYIGV K	IP / COS-7	(Scheer, Costa et al. 2000)
A1AB_human	α_{1B} -adrenergic		TMIII carboxyl end of IC3 TMV		128 AVDVLCTASI F 293 REKKA A KTLLGI E 204 EPPFYALFSSLG V	IP / COS-1 IP arachidonic acid release IP / COS-1	(Perez, Hwa et al. 1996) (Hwa, Gaivin et al. 1997)
A1AB_human	α_{1B} -adrenergic		C-terminal IC3		293 SREKKA A KT X=19 different substitutions	PI / COS-7	(Kjelsberg, Cotecchia et al. 1992)
A1AB_human	α_{1B} -adrenergic		C-terminus IC3		288 293 KFSREKKA A KTLLGI K H L	PI hydrolysis / rat fibroblast	(Allen, Lefkowitz et al. 1991)
A2AA_human	α_2C10 -adrenergic alpha-2AAR		C-terminal IC3 loop		373 (348?) EKRF T FVLAV X=F, A, C, E, K	adenyl cyclase inhibition / HEK293	(Ren, Kurose et al. 1993)
ACM1_human	muscarinic Hm1 muscarinic acetylcholine M1		C-terminal IC3 loop junction		360 SLVKEKKAARTLS A	PI / HEK(U293)	(Högger, Shockley et al. 1995)
ACM2-human	muscarinic acetylcholine M2		junction of IC3 and TMVI		390 KKVTRTIL 1 A 1-4 A inserted	IP production, inhibition of cAMP production / COS-7	(Liu, Blin et al. 1996)

Figure 1 (Page 2 of 15)

CLASS A GROUP II			TMVI					
ACM3_rat	m3 muscarinic (rat)		TMVI			507 TWTPYNIMVLVNT S	IP / COS-7	(Blüml, Mutschler et al. 1994)
ACM5_human	muscarinic acetylcholine M3 m5 muscarinic		N-terminus to TMII TMVI			chimera composed of m2 1-69 m5 77-445 m2 391-466	β -gal / NIH 3T3	(Burststein, Spalding et al. 1996)
ACM5_human	muscarinic acetylcholine M5 m5 muscarinic		TMVI			451 459 465 AILLA FLITW TPYNI MVLVST M L H C V S F T	β -gal; radioligand binding / NIH-3T3	(Spalding, Burststein et al. 1998)
ACM5_human	muscarinic acetylcholine M5 m5 muscarinic		junction of TMVI and EC3			465 YNIMVLVSTFCDKCV X=V,F,R,K,+more	β -gal; radioligand binding / NIH-3T3	(Spalding, Burststein et al. 1997)
B1AR_human	β_1 -adrenergic		C-terminus			389 RKAFOGLLCCA R	adenylyl cyclase; agonist binding / CHW	(Mason, Moore et al. 1999)
B2AR_human	β_2 -adrenergic beta-2AR		C-terminal IC3 loop			266 272 FCLKEHKALKTLGI SR K A	adenylyl cyclase activation; agonist binding affinity / COS-7 or CHO	(Samama, Cotecchia et al. 1993); (Lefkowitz, Cotecchia et al. 1993)
DADR_human	dopamine D1A		carboxyl terminal IC3			264 SFKMSEKRETKVLKT I K 288 from D1B receptor APDTSIKKETKVLKT	adenylyl cyclase; cAMP accumulation / HEK293	(Charpentier, Jarvie et al. 1996)
DADR_human	dopamine D1		TMVI			286 FVCCWLPPFFIL A	CAMP accumulation / COS-7	(Cho, Taylor et al. 1996)
HH2R_rat	histamine H ₂		IC2			115 FMISLDRYCAV N, A	cAMP production / HEK-293	(Alewijnse, Timmerman et al. 2000)

Figure 1 (Page 3 of 15)

File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS A GROUP III					
OPSD_human	opsin	TMII	90 FMVLGGFTSTLY D	transducin; phosphorylation by rhodopsin kinase / COS	(Rim and Oprian 1995)
	rhodopsin	TMIII	113 GCNLEGGFFAT Q		
		TMVII	292 296 MTIPAFFAKSAAIY E G, E, M 292Ala neutral a.a converted to carboxylate and competes with ¹¹³ Glu for salt bridge with ²⁹⁶ Lys		
OPSD_human	opsin	TMIII	134 VVLAIERYVVV I, Q, S	transducin; radioligand binding / COS	(Acharya and Karnik 1996)
OPSD_human	rhodopsin	TM6	257 RMVIMVIAFL Y, N	transducin, GTP γ S uptake / COS	(Han, Smith et al. 1998)
OPSD_human	opsin	plus TM3 TMVII	plus G113Q 296 PAFFAKSAAIY G X=E,M natural mutants + 10 different a.a. substitutions disrupts critical salt bridge between ²⁹⁶ Lys(TMVII) and ¹¹³ Glu(TMIII)	transducin; radioligand binding / COS	(Govardhan and Oprian 1994); (Cohen, Yang et al. 1993)
	rhodopsin	IC2	134 VVLAIERYVVV Q		(Cohen, Yang et al. 1993)

Figure 1 (Page 4 of 15)

TRFR_mouse	thyrotropin-releasing hormone TRH-R	carboxyl tail	³³⁵ FRKL C NCCKQK STOP	⁴⁵ Ca ²⁺ efflux, [Ca ²⁺] / Xenopus oocytes: IP formation / AIT20, <i>stably transfected</i>	(Matus-Leibovitch, Nussenzveig et al. 1995)

TMIII
TMVI

File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS A GROUP IV BRB2_human	bradykinin B ₂ B2 bradykinin BK-2	TMIII TMVI	113 AIIISM N LYSSI A 256 LLFIICWLPFQI F	IP production / COS-7	(Marie, Koch et al. 1999)

Figure 1 (Page 6 of 15)

File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS A GROUP V					
AG2R_rat	AT _{1A} Type-1A angiotensin II	TMIII	111 ASVSFNLVASV A disrupts ¹¹¹ Asn(TMIII) - ¹¹² Tyr(TMVII) interaction	phospholipase C; IP production / COS-7	(Grobowski, Maigret et al. 1997)
AG2R_rat	AT _{1A}	C-terminus of TM7	305 LFYGF L GKKFK Q	IP production / HEK-293; intracellular Ca ²⁺ mobilization / CHO	(Pamot, Bardin et al. 2000)
FMLR_human	Type-1A angiotensin II formylmethionylleucylphenylalanine (fMLPR)	other multiple mutations IC1	51 LVIVWAGFRMTHTVTTISYLNKAVA LVVWVTAFEA K RTINAIWFLNLAVA (K above conflicts with SWISS-PROT database)	PI production; phospholipase C stimulation / COS-7	(Amatruda, Dragas-Graonic et al. 1995)
IL8B_human	interleukin-8 receptor B	IC2	138 ACISV D RYLAIVH V	IP production; Ca ²⁺ mobilization and actin polymerization / NIH 3T3	(Burger, Burger et al. 1999)
LSHR_human	CXCR-2 chemokine	IC3	564 MATNK D TKIAKK G	cAMP production / HEK293	(Kudo, Osuga et al. 1996)
LSHR_human	luteinizing hormone (LH)	TMVI	578 ILIFT D FTCMA G	cAMP production / COS-7	(Shenker, Laue et al. 1993)
LSHR_human	luteinizing hormone (LH)	TM6	571 577 KIAKK M AILIFT D FTCM I I	cAMP production / COS-7	(Kosugi, Van Dop et al. 1995)
LSHR_rat	luteinizing hormone / human chorionic gonadotropin (LH/hCG)	TMVI	556 ILIFT D FTCMA G, Y	cAMP production / HEK 293T	(Bradbury, Kawate et al. 1997; Bradbury and Menon 1999)
OPRD_mouse	delta opiod receptor	TM3	128 KVLSID I YNNMF A, K, H	adenyl cyclase inhibition / COS-7	(Cavalli, Babey et al. 1999)
OXYR_human	oxytocin	IC2	137 LMSLD R CLAIC A	IP production / COS-7	(Fanelli, Barbier et al. 1999)

Figure 1 (Page 7 of 15)

PAFR_human	platelet-activating factor (PAF)	C-terminus of IC3	231 EVKRRAL ^R WMVCTVLAV	IP production / COS-7	(Parent, Le Gouill et al. 1996)
PAFR_human	platelet-activating factor (PAF)	TMIII	100 CLFFINTYCSV ^A	arachidonate release, IP production, adenylyl cyclase inhibition / CHO	(Ishii, Izumi et al. 1997)
PE23_human	prostaglandin E ₃ , EP3III EP3IV	C-terminal tail	360 FCQEEFWGN FCQMRKRRRLREOEFWGN ↑truncated	inhibition of adenylyl cyclase / CHO-K1	(Jin, Mao et al. 1997)
PE23_mouse	prostaglandin E ₃ EP3	carboxyl-terminal tail	336 KILLRKFCQIRDHT (3α) MMNHL (3β) ↑truncated	inhibition of adenylyl cyclase / CHO, <i>stably expressed</i>	(Hasegawa, Negishi et al. 1996)
THRR_human	thrombin	EC2 loop	259 268 CHDVINETLLEGGYAYV DLKD KDF I	⁴⁵ Ca ²⁺ efflux, PI hydrolysis, reporter gene induction / COS-7	(Nanevich, Wang et al. 1996)
TSHR_human	thyrotropin (TSHR) thyroid stimulating hormone	EC1	486 YYNHAIWDQGTG F, M	inositol phosphate-- diacylglycerol cascade / COS-7	(Parma, Van Sande et al. 1995)
		EC2	568 YAKVSICLPMD T		
TSHR_human	thyrotropin (TSHR) thyroid stimulating hormone	TMIII	509 ASELSVYTLTV A	adenylyl cyclase activation / COS-7	(Duprez, Parma et al. 1994)
		TMVII	672 YPLNSCANPFL Y		
TSHR_human	thyrotropin (TSHR)	TMV	597 VAFVIVCCCHV L	cAMP formation / COS-7 cells	(Esapa, Duprez et al. 1999)
TSHR_human	thyroid stimulating hormone thyrotropin (TSHR)	TMVII	677 CANPFLYAIFT V	cAMP formation / CHO cells	(Russo, Wong et al. 1999)
TSHR_human	thyroid stimulating hormone thyrotropin (TSHR)	IC3	613 621 VRNPOYNPGDKDTKIAK deletion	cAMP formation / COS-7	(Wonerow, Schoneberg et al. 1998)

Figure 1 (Page 8 of 15)

TSHR_human	thyrotropin (TSHR)	IC3 / TMVI	623 632 KDTKIARMAVLIFTDFICM V I	cAMP activation / COS-7	(Paschke, Tonacchera et al. 1994)
V2R_human	thyroid stimulating hormone vasopressin V2	IC2	136 LMTLDHRRAI A	cAMP formation / COS-7	(Morin, Cotte et al. 1998)

File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS B GROUP I					
CALR_human	human calcitonin hCTR-1 hCTR-2	wild type (native) protein		adenylyl cyclase cAMP production / COS-1	(Cohen, Thaw et al. 1997)
CLASS B GROUP II					
PTRR_human	parathyroid hormone. PTH / PTH-related peptide	junction of IC1 and TMII junction of IC3 and TMVI	223 TRNYIH M HLFL R, K 410 KLLKST L VLMP C, others	cAMP accumulation / COS-7	(Schipani, Jensen et al. 1997)
CLASS B GROUP III					
GIPR_human	glucose-dependent insulinotropic peptide (GIP-R)	TMVI	340 VFAPV T EEQAR P	cAMP production / L293	(Tseng and Lin 1997)
GLR_rat	glucagon	junction of IC loop I and TMII IC end of TMVI	178 TRNYIH G NLFA R 352 RLARST L TLIP A	cAMP accumulation / COS-7	(Hjorth, Orskov et al. 1998)
VIPR_human	vasoactive intestinal peptide 1 (VIP)	junction of IC loop 1 and TMII junction of IC loop 3 and TMVI	178 RNYIH M HLFI R requires functional integrity of the N-terminal EC domain 343 LARST L LLIP X= K, P	cAMP production / COS-7 or CHO	(Gaudin, Maoret et al. 1998) (Gaudin, Rouyer-Fessard et al. 1998)

Figure 1 (Page 10 of 15)

File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS D					
O74283 RCB2 C. cinereus	pheromone	TM6	229 PLSAYQIYLGT P	heterologous yeast assay	(Olesnicky, Brown et al. 1999)
STE2_yeast	pheromone α -factor	TM6	258 QSLVPSIIFI LL	<i>lacZ</i> reporter gene	(Konopka, Margarit et al. 1996)
STE2_yeast	pheromone α -factor	double mutations TM5 and TM6	223 MSFVLVVKILAIR C C 247 251 DSFHILLVSCQSLL CC CC double mutations TM5 and TM6	<i>lacZ</i> reporter gene / yeast	(Dube, DeCostanzo et al. 2000)
STE3_yeast	pheromone α -factor	IC3	194 DVRDILHCTNS Q	β -galactosidase	(Boone, Davis et al. 1993)
STE2_yeast	pheromone α -factor	TM6	253 258 LIMSCQSLLVPSIIFI L LP	β -galactosidase	(Sommers, Martin et al. 2000)

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Light Emission Induced by the WT CCK-BR vs. a Constitutively Active Mutant

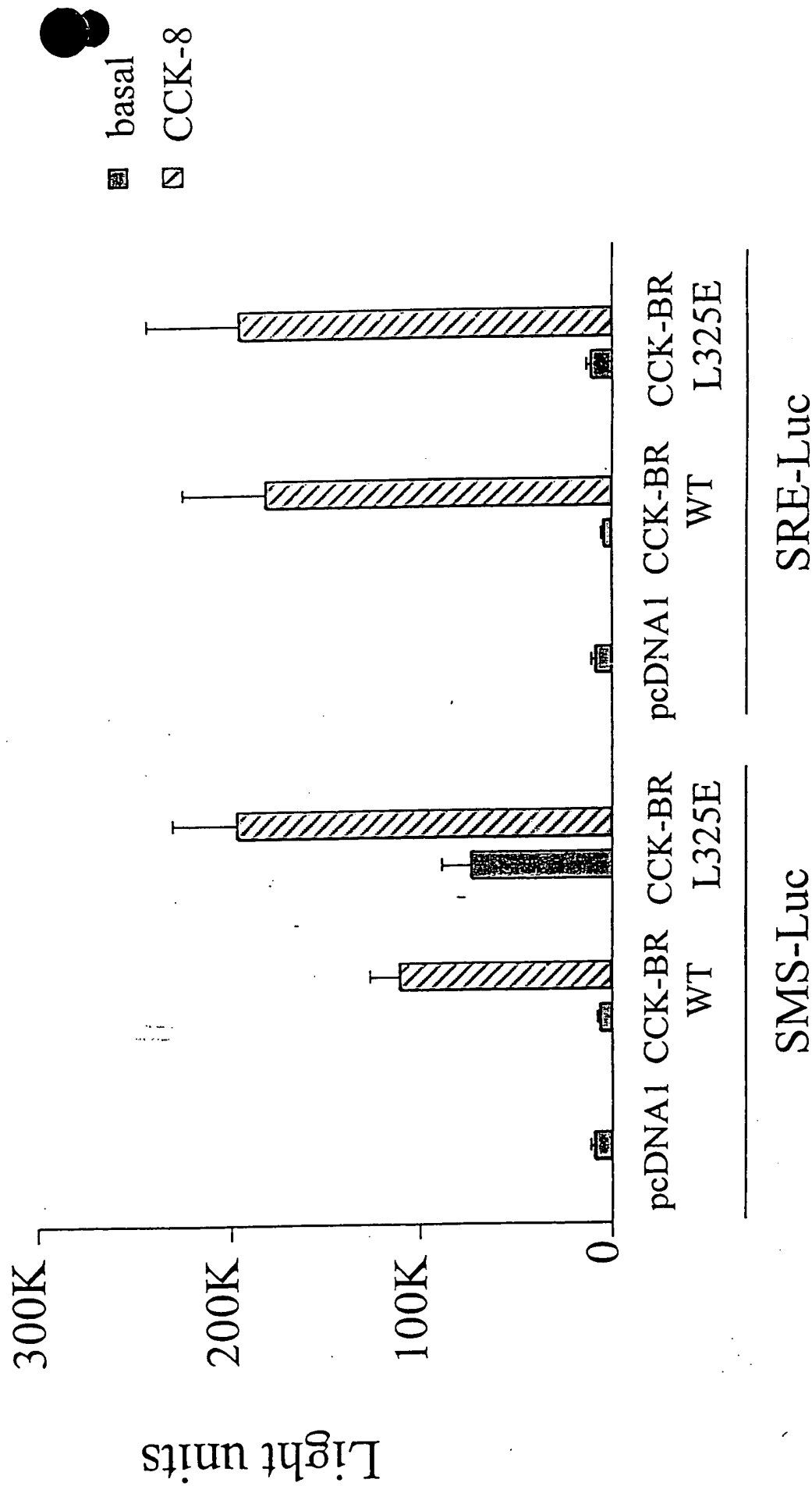


Figure 2

A Point Mutation Confers Constitutive Activity to the Rat μ Opioid Receptor

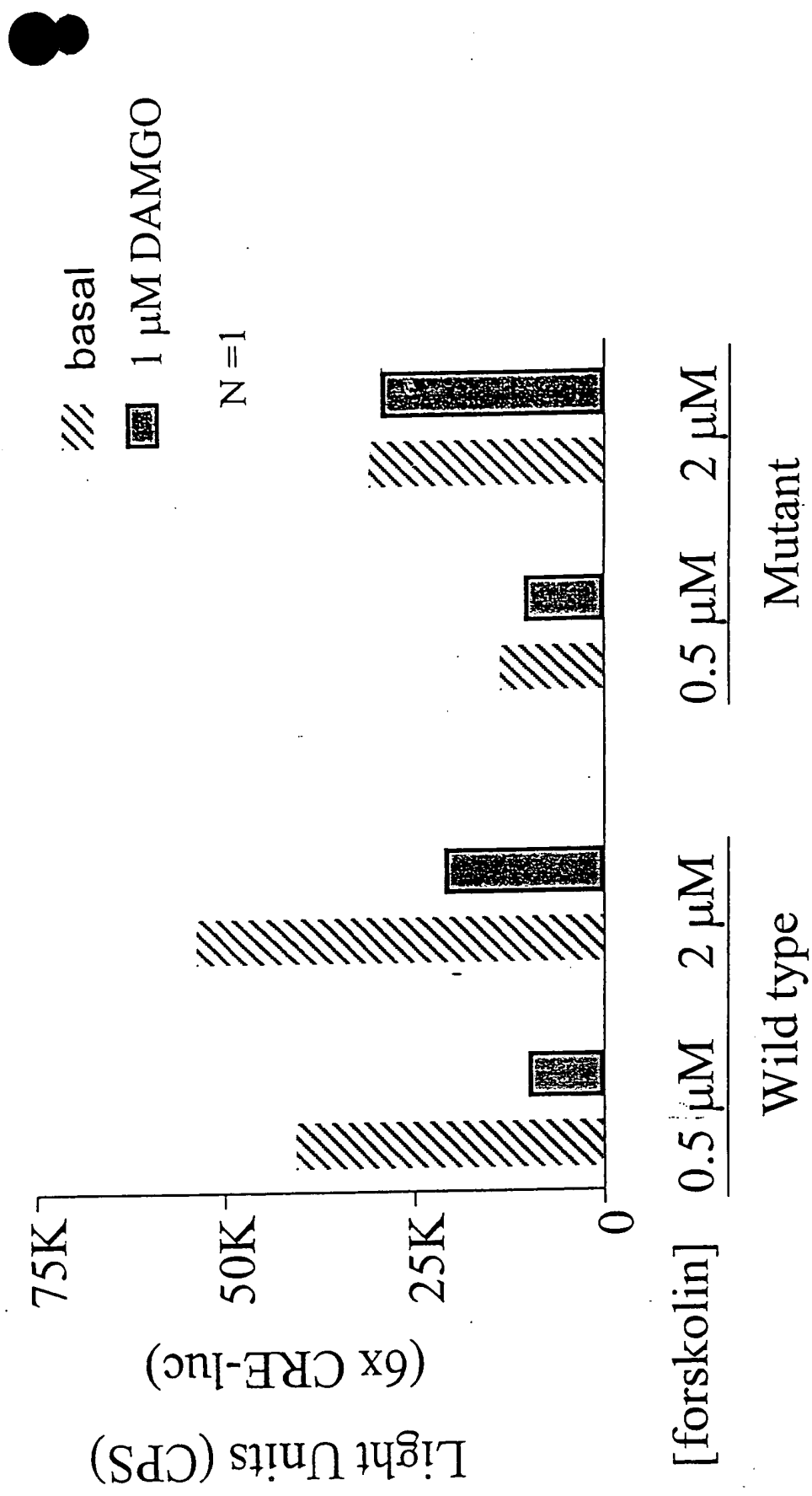


Figure 3

Forskolin Stimulated HEK293 Cells Transfected With pcDNA1 and a CRE-luc Construct

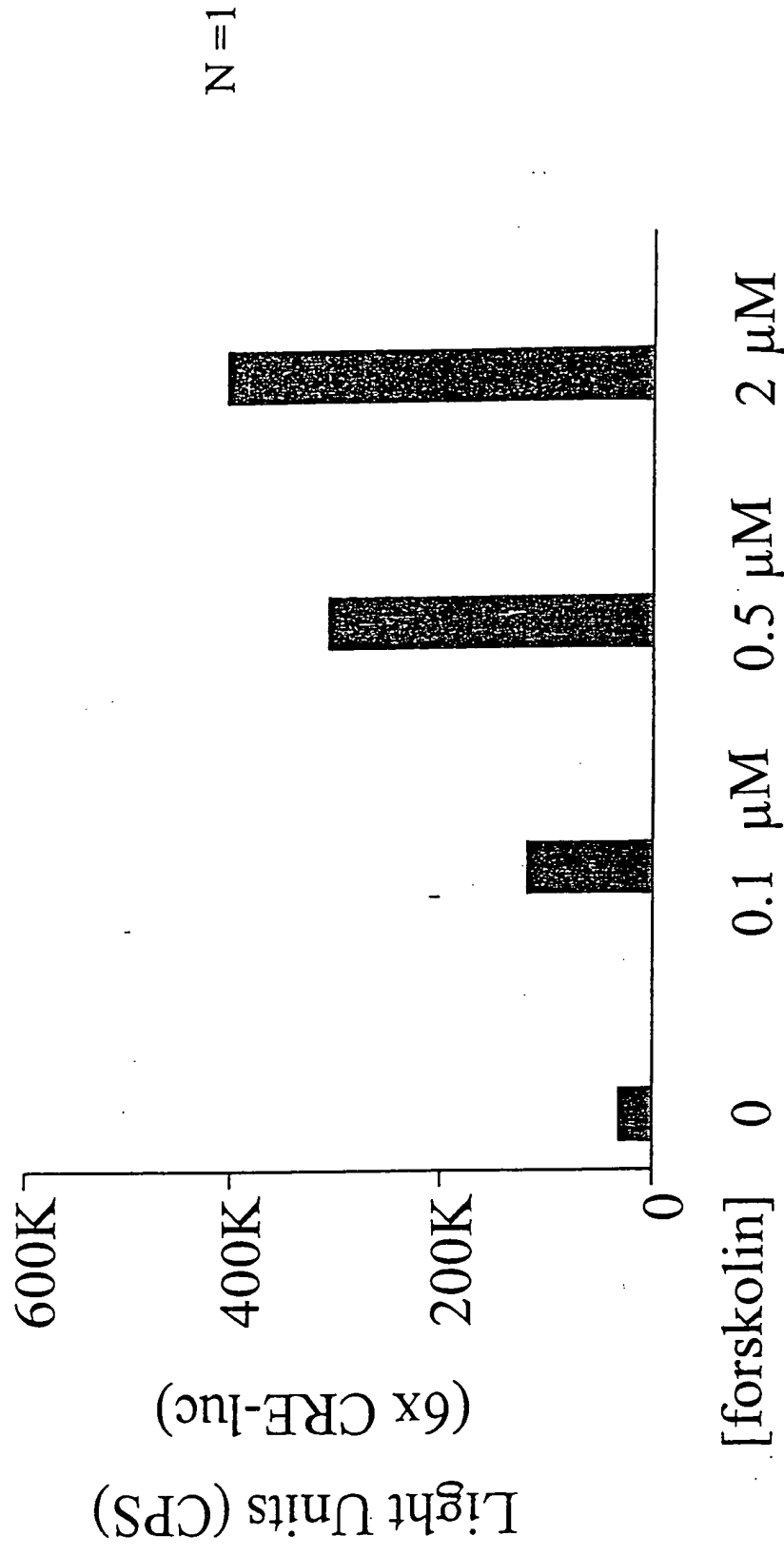


Figure 4

The Rat μ Opioid Receptor Signals Through G α i



Figure 5

A Point Mutation Confers Constitutive Activity to the Rat μ Opioid Receptor



Figure 6

Target Residues Within Class I GPCRs

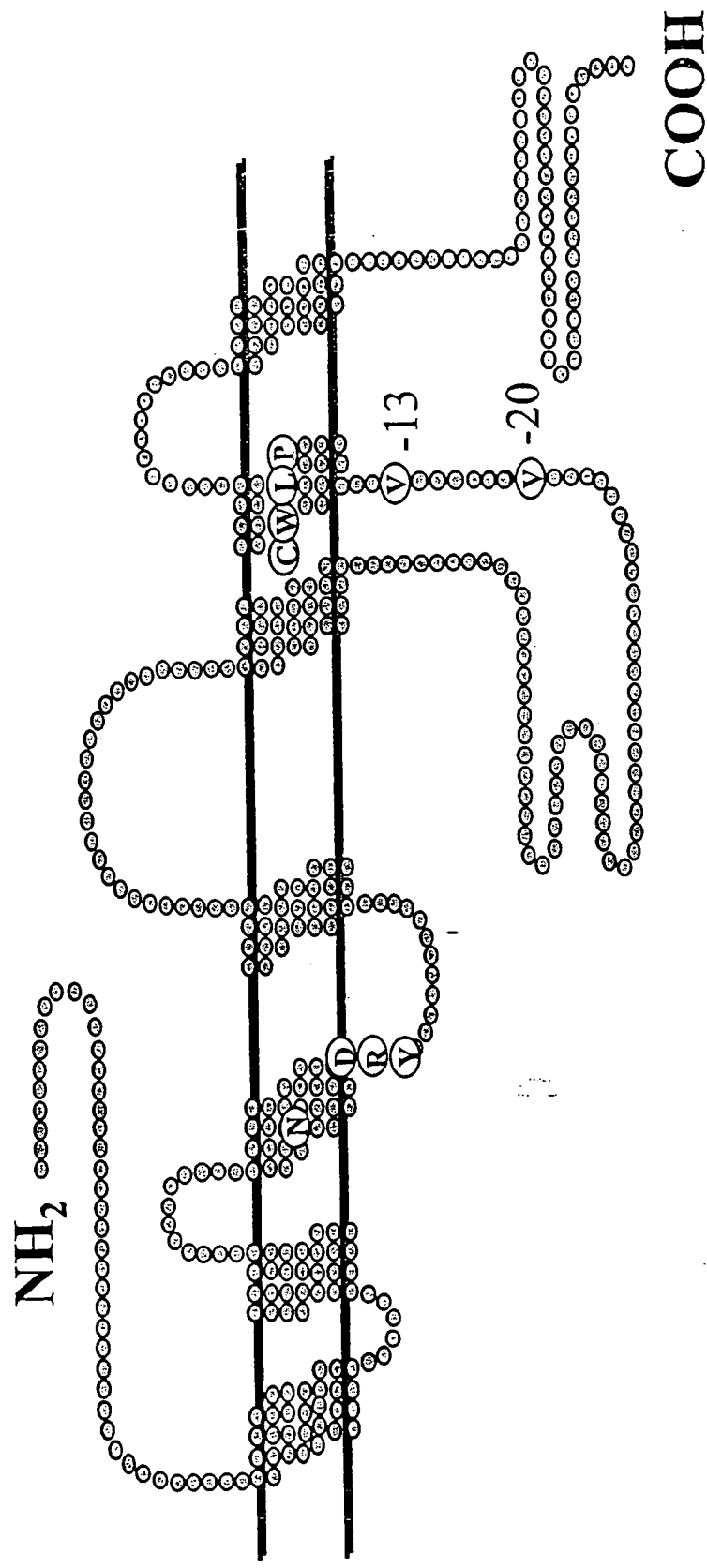


Figure 7

TMD III Asn (-14 from DRY) is a Target for Mutation Induced Constitutive Activity

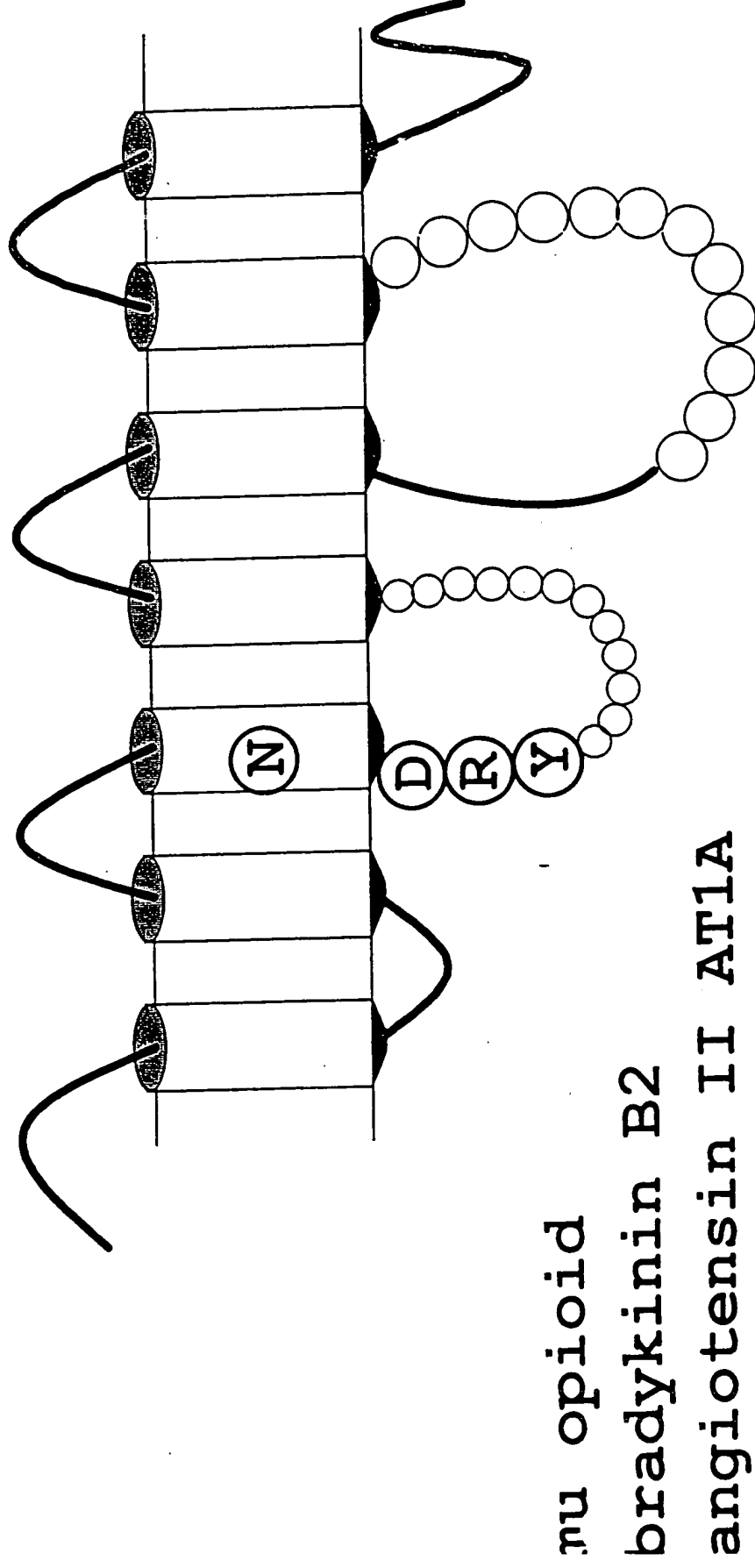


Figure 8

The 'DRY' Motif is a Target for Mutation Induced Constitutive Activity

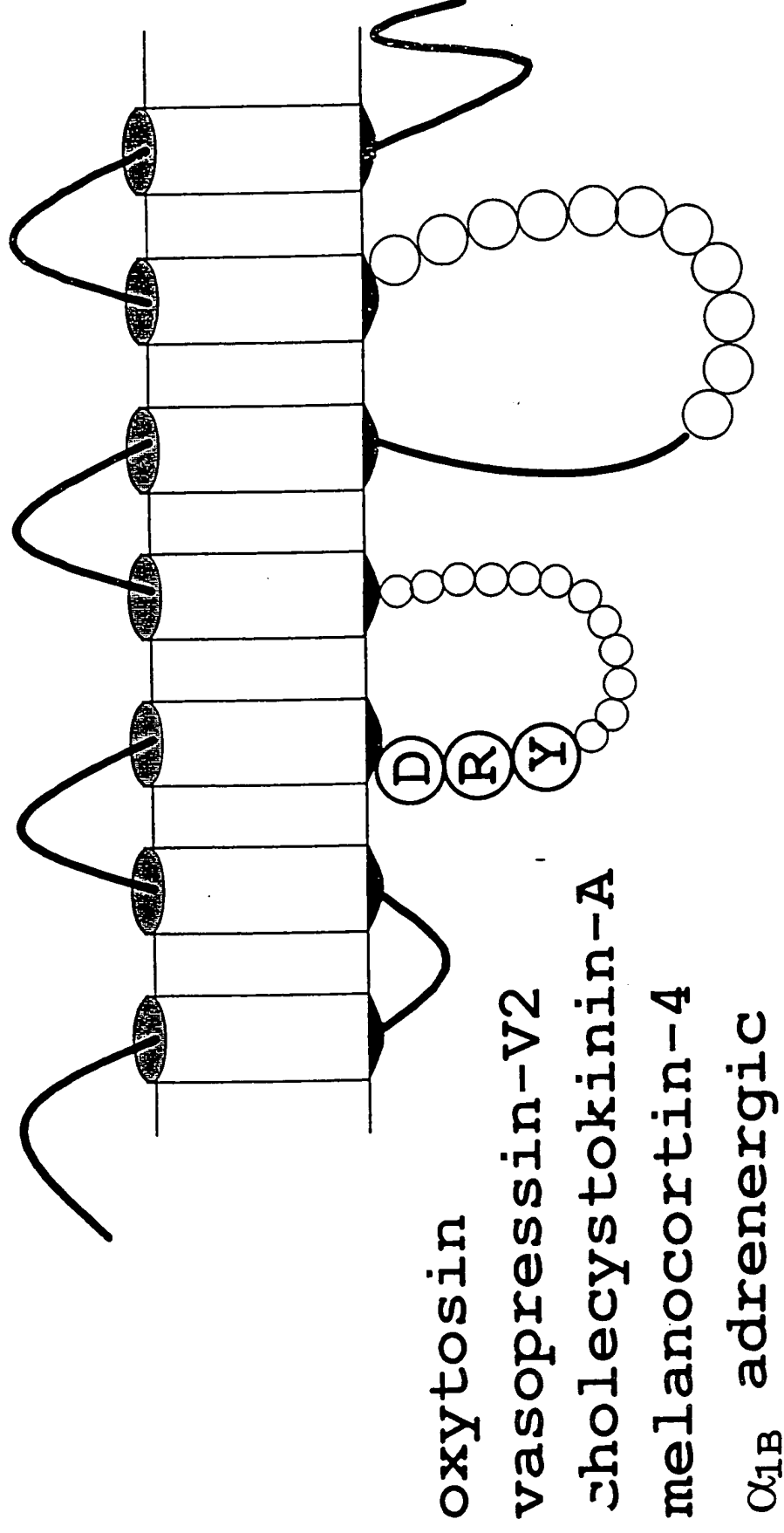


Figure 9

A Point Mutation Enhances MC-4 Receptor Constitutive Activity

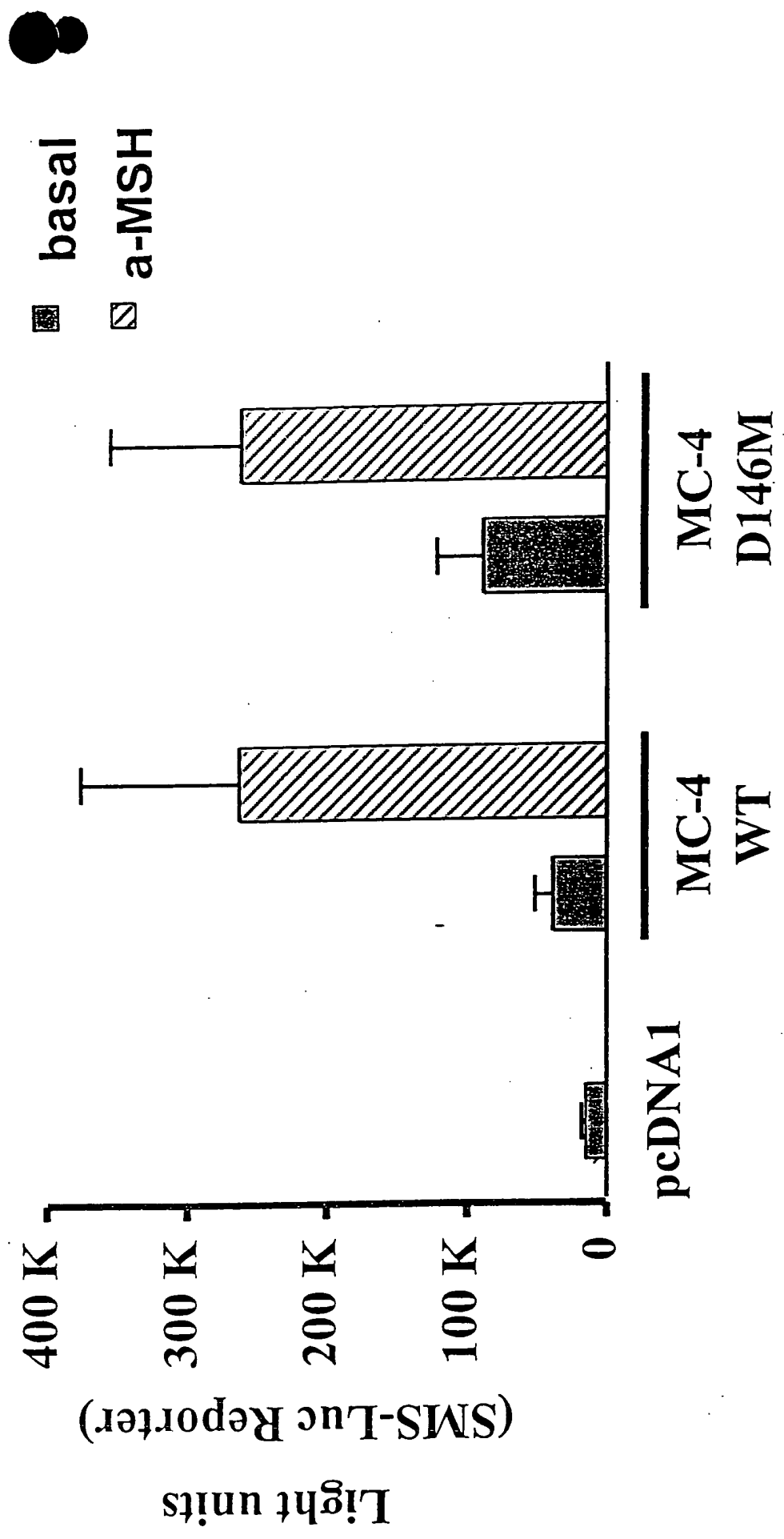


Figure 10

The -13 Position is a Target for Mutation Induced Constitutive Activity

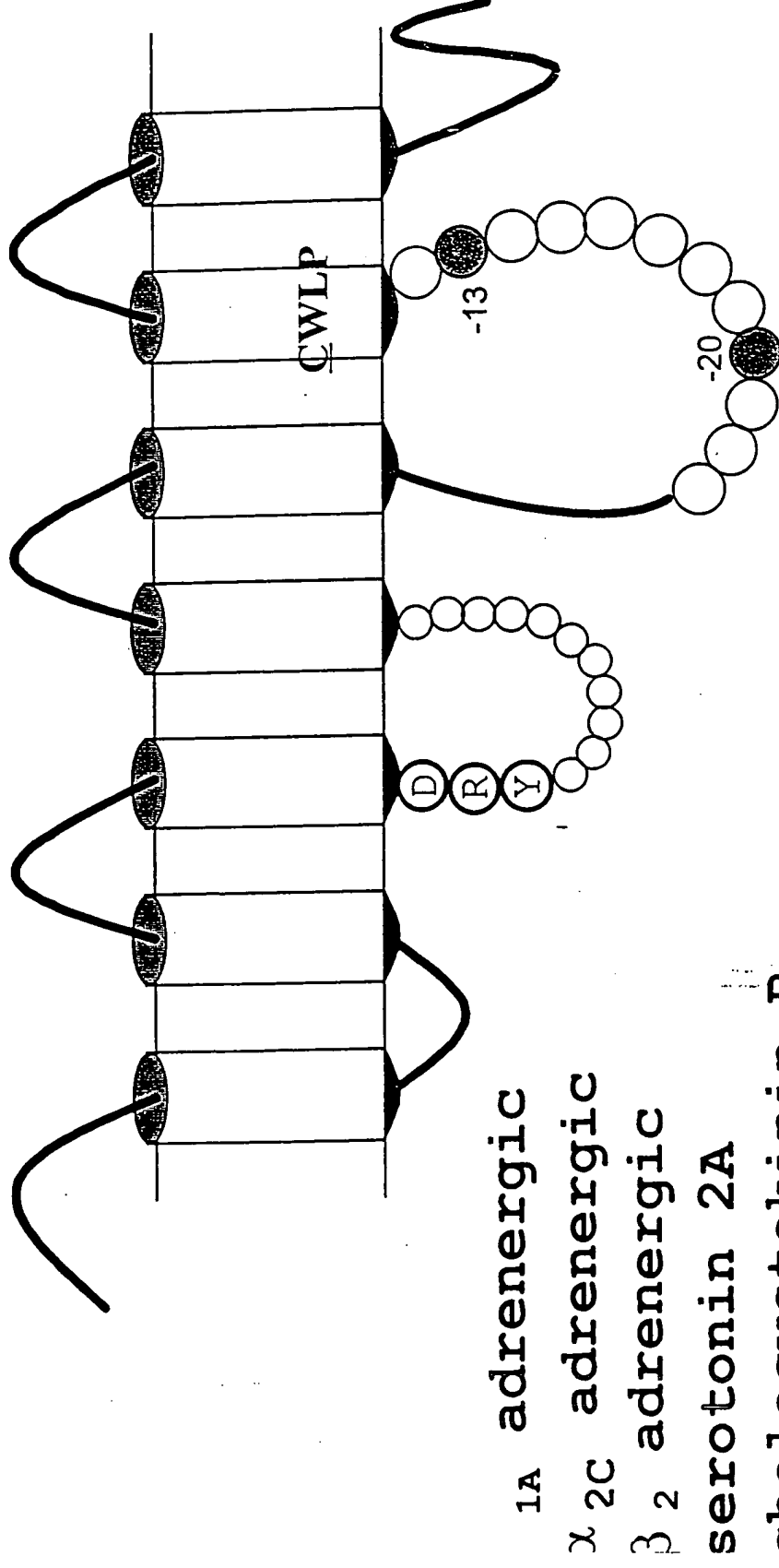


Figure 11

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ork 1 -----ME-----FRGEPGPTCAPSACLPNMSAWFPWASP.....NGSAGSSEDAQ
orkr 1 -----MESPIQIFRGEPTCAPSACLPNMSAWFPWASP.....DSNGSVGSSEDOQ
orm 1 MDSSAAPTNASNCTDAEAYSSCSAPSPGSGW...NLSHLDGMLSDPCGNRTDLGGDRSL
ormr 1 MDSSTGPGNTSDCSDPEAQASCSPA...EGSW...NLSHVDGMOQSDPCGLNRTGLGGNDL
ord 1 -----MEPAPSAGABL...Q.PPLFAMASDAYPSACPSAGANASG
AT1a 1 -----MALNSSAEDGIKRIQ
BK-2 1 -----MFSPWKISMFLSVREDSVPTTASFSALMLNVTLOQPTLNG.TFAQ

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ork 49 LEPAHISEAH...PZHITAMYSVFEVVGILVGNLSVMEVTHRYTKMKTATNIYIFNLALADA
orkr 49 LEPAHISEAH...PZHITAMYSVFEVVGILVGNLSVMEVTHRYTKMKTATNIYIFNLALADA
orm 59 CPPTGS.PSMITATIMALKSHVGVGILVGNLSVMEVTHRYTKMKTATNIYIFNLALADA
ormr 57 CPQTGS.PSMVTATIMALKSHVGVGILVGNLSVMEVTHRYTKMKTATNIYIFNLALADA
ord 37 PPGARSASSIALAHITALLYSAVCAVGLVGNLSVMEVTHRYTKMKTATNIYIFNLALADA
AT1a 16 DDCPRAGRHSYIFVHPTLYSHVGVGILVGNLSVMEVTHRYTKMKTATNIYIFNLALADL
EK-2 45 SKCPQVEWLGWLNTHQPPFLWVFEVATTEMIFVLSVFLCHKSSCTVAE...LYLGNLAADL

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ork 107 LVTHITPEOSTVYLMN...SWPFGHILCKIVISIDYIMETSIFTLTMSVDRYIAVCHPVK
orkr 107 LVTHITPEOSTVYLMN...SWPFGHILCKIVISIDYIMETSIFTLTMSVDRYIAVCHPVK
orm 118 LATSILPEOSTVYLMN...SWPFGHILCKIVISIDYIMETSIFTLTMSVDRYIAVCHPVK
ormr 116 LATSILPEOSTVYLMN...SWPFGHILCKIVISIDYIMETSIFTLTMSVDRYIAVCHPVK
ord 97 LATSILPEOSTVYLMN...SWPFGHILCKIVISIDYIMETSIFTLTMSVDRYIAVCHPVK
AT1a 76 CFLLLPLWAVYTAMEYRMDPCNHLCKIASASVTENTYASMEILYICLSDRYIAVCHPVK
BK-2 105 ILACGLPEWATITISNNFDWLEGETLCKIVISIDYIMETSIFTLTMSVDRYIAVCHPVK

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↑ from DAY *

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ork 166 ALDERTPLKAKLINICHWLLSSVCHSALVLCGTVR...EDVDVIECSLOFPDDDDYSWWD
orkr 166 ALDERTPLKAKLINICHWLLSSVCHSALVLCGTVR...EDVDVIECSLOFPDDEYSWWD
orm 177 ALDERTERNAKLINICHWLLSSVCHSALVLCGTVR...Q...GSIDCHLTFSHPTW...YWE
ormr 175 ALDERTERNAKLINICHWLLSSVCHSALVLCGTVR...Q...GSIDCHLTFSHPTW...YWE
ord 156 ALDERTPAKAKLINICHWLLSSVCHSALVLCGTVR...D...GAVVOMLOFPSPSW...YWD
AT1a 136 SRLRRITMLVAKTCHIIHMLAGLASIPAVIHRNV...YFIENTNITVCAFHYESRN.STLP
BK-2 165 MGRMRGVRWAKYSLVINGCILLSSPVVFRMTKEYSDEGHNVTAQVISYPS...LIWE

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ork 224 LFMKICVFIFAFVLPVLIITVCYGLMILRLKSVRLSGSHEKDRNLRRITRVLVWVAVF
orkr 224 LFMKICVFIFAFVLPVLIITVCYGLMILRLKSVRLSGSHEKDRNLRRITRVLVWVAVF
orm 232 NLKICVFIFAFVLPVLIITVCYGLMILRLKSVRLSGSHEKDRNLRRITRVLVWVAVF
ormr 230 NLKICVFIFAFVLPVLIITVCYGLMILRLKSVRLSGSHEKDRNLRRITRVLVWVAVF
ord 211 TVTKICVFIFAFVLPVLIITVCYGLMILRLKSVRLSGSHEKDRNLRRITRVLVWVAVF
AT1a 193 IGLGELTKNILGFLFFPLIITTSYTLTWKALKKAYEIOKNKPRNDD...IFRIMAVLFF
BK-2 222 VFTNMLLNVLVGLFIP.LSVITFCVMOHMOVLRRNEMOKFKEIQTE.RRATVVLVVLFF

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ork 284 IVCWTPDHIFLIVVHALGS.T....SHSTAALSSMYFCIALGYTNSCLNPVLYAFDENE
orkr 284 IVCWTPDHIFLIVVHALGS.T....SHSTAALSSMYFCIALGYTNSCLNPVLYAFDENE
orm 292 IVCWTPDHIFLIVVHALGS.T....SHSTAALSSMYFCIALGYTNSCLNPVLYAFDENE
ormr 290 IVCWTPDHIFLIVVHALGS.T....SHSTAALSSMYFCIALGYTNSCLNPVLYAFDENE
ord 271 IVCWTPDHIFLIVVHALGS.T....SHSTAALSSMYFCIALGYTNSCLNPVLYAFDENE
AT1a 250 FFSWVBEHOLETFIDVLIQLGVIHDCIKSDIVDTAMPITICLAYFNNCLNPLFYGLGKKE
BK-2 280 IVCWTPDHIFLIVVHALGS.T....SHSTAALSSMYFCIALGYTNSCLNPVLYAFDENE

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SEQ ID NO:

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ork 338 KRCFRIFCFEIKMERMEROSTSRIR.NTVOD.PAYLRDIDGMKPV----- 76
orkr 338 KRCFRIFCFEIKMERMEROSTSRIR.NTVOD.PASMRDVGGMKPV----- 77
orm 346 KRCFRIFCFEIKMERMEROSTSRIR.NTVOD.PASMRDVGGMKPV----- 78
ormr 344 KRCFRIFCFEIKMERMEROSTSRIR.NTVOD.PASMRDVGGMKPV----- 79
ord 326 KRCFRIFCFEIKMERMEROSTSRIR.NTVOD.PASMRDVGGMKPV----- 80
AT1a 310 KRYLQLLKYIPPAKSHS...SLSTKM..STLSYRPSDNMSSAKKPASCFEVE- 81
BK-2 340 RKKSWVYQGVQGGCRSEPIQMENS..GTL..RTSISVEROIHKLQDWAGSRQ 82

```

Figure 12

mORmouse 1 MDSSAGEGNISDCSDPLA.PASCSIPA...ECSTWMLSHVDGNOSDPOGPNRTGLGCSHSLC
mORrat 1 MDSSAGEGNISDCSDPLA.QASCSIPA...ECSTWMLSHVDGNOSDPOGPNRTGLGCSHSLC
mORbovin 1 MDSCAVETNASNCHDEFTHPSSCSPPSPSSSWANFSLHLEGNLSDPOGPNRTGLGCSHSLC
mORhuman 1 MDSSAGEGNISDCSDPLA.PASCSIPA...ECSTWMLSHVDGNOSDPOGPNRTGLGCSHSLC
mORpig 1 MDSSAGEGNISDCSDPLA.PASCSIPA...ECSTWMLSHVDGNOSDPOGPNRTGLGCSHSLC
mORws 1 MMS...GNISDFLYPLS...NEVMS...NSSVLGRNFSNSTSLNMGSSRDSTD
ATla 1 -----MALNSSAEDGKRIQDDC
BK-2 1 -----MFSWIKISMFLSVREDSVPTTASFADMLNVTLOETLNG.TFACSKC

mORmouse 58 EOTGSPSMYTAITINALYSIVCVGLGFLMVMVIVRYTKMTATNTYIENLALADALA
mORrat 58 EOTGSPSMYTAITINALYSIVCVGLGFLMVMVIVRYTKMTATNTYIENLALADALA
mORbovin 61 ESAGSPSMYTAITINALYSIVCVGLGFLMVMVIVRYTKMTATNTYIENLALADALA
mORhuman 60 EOTGSPSMYTAITINALYSIVCVGLGFLMVMVIVRYTKMTATNTYIENLALADALA
mORpig 61 EOTGSPSMYTAITINALYSIVCVGLGFLMVMVIVRYTKMTATNTYIENLALADALA
mORws 48 EOKTE...ITIALIITTLYSIVCVGLGFLMVMVIVRYTKMTATNTYIENLALADALA
ATla 19 EKAGRHSYIFVM.IPTLHSIFVWGLGFLMVMVIVRYTKMTATNTYIENLALADALA
BK-2 48 EOVEWLGNITL.OPPFLWVIFVETLENI FVLSVFLHKSSCIVAEIVYGNLAADLIL

mORmouse 118 ESTLPEFSVNYLMG.TWPEGTILCKIVISIDYNNMFTSIPTLCTMSVDRYIAVCHPVKAL
mORrat 118 ESTLPEFSVNYLMG.TWPEGTILCKIVISIDYNNMFTSIPTLCTMSVDRYIAVCHPVKAL
mORbovin 121 ESTLPEFSVNYLMG.TWPEGTILCKIVISIDYNNMFTSIPTLCTMSVDRYIAVCHPVKAL
mORhuman 120 ESTLPEFSVNYLMG.TWPEGTILCKIVISIDYNNMFTSIPTLCTMSVDRYIAVCHPVKAL
mORpig 121 ESTLPEFSVNYLMG.TWPEGTILCKIVISIDYNNMFTSIPTLCTMSVDRYIAVCHPVKAL
mORws 107 ESTLPEFSVNYLMG.TWPEGTILCKIVISIDYNNMFTSIPTLCTMSVDRYIAVCHPVKAL
ATla 78 LITLLEWVYTAMEYRWPCNHLCKIASASVTENYASVELLTCESIDRYIAVCHPVKSR
BK-2 107 ACGLPEWATTISNNFDMLPGETLORVNIISNNLYSSICFLMLVSDRYIAVCHPVMSMG

mORmouse 177 DFRTPRNAKINVCNWLSSAIGLPVMFMATTKYRO.....GSIDCTLTFSHPTWYWE
mORrat 177 DFRTPRNAKINVCNWLSSAIGLPVMFMATTKYRO.....GSIDCTLTFSHPTWYWE
mORbovin 180 DFRTPRNAKINVCNWLSSAIGLPVMFMATTKYRO.....GSIDCTLTFSHPTWYWE
mORhuman 179 DFRTPRNAKINVCNWLSSAIGLPVMFMATTKYRO.....GSIDCTLTFSHPTWYWE
mORpig 180 DFRTPRNAKINVCNWLSSAIGLPVMFMATTKYRO.....GSIDCTLTFSHPTWYWE
mORws 166 DFRTPRNAKINVCNWLSSAIGLPVMFMATTKYRO.....GSIDCTLTFSHPTWYWE
ATla 138 LRRIMLVAKYTCIIIMVAGLASLEAVIHRNV....YFIENTNITVCAFHVESRNSTLP
BK-2 167 RMRGVWAKLYSLVWGCTLLSSPMLVFRIMK...EYSDEGHNVTA CVLSYPS..LIWE

mORmouse 230 NLLKICVFIFAFIMPVLLITVCGMLILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVF
mORrat 230 NLLKICVFIFAFIMPVLLITVCGMLILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVF
mORbovin 233 NLLKICVFIFAFIMPVLLITVCGMLILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVF
mORhuman 232 NLLKICVFIFAFIMPVLLITVCGMLILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVF
mORpig 233 NLLKICVFIFAFIMPVLLITVCGMLILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVF
mORws 226 TLKICVFIFAFIMPVLLITVCGMLILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVF
ATla 193 IGLGKTNLGLGFFHLLTSTYTLWKAUKKAYEIKOKNPEPND...IFRILIAVILFF
BK-2 222 VFTNMLINNVGLLEP.LSVITFCTMOIMOVLRNNEOKFKEIOTE.RRATVGLVWLITE

mORmouse 290 IVCWTPIHIVLIKALITI.....PETTFOTVSWHFCIALGYTNSCLNPVLYAFLDENF
mORrat 290 IVCWTPIHIVLIKALITI.....PETTFOTVSWHFCIALGYTNSCLNPVLYAFLDENF
mORbovin 293 IVCWTPIHIVLIKALITI.....PETTFOTVSWHFCIALGYTNSCLNPVLYAFLDENF
mORhuman 292 IVCWTPIHIVLIKALITI.....PETTFOTVSWHFCIALGYTNSCLNPVLYAFLDENF
mORpig 293 IVCWTPIHIVLIKALITI.....PETTFOTVSWHFCIALGYTNSCLNPVLYAFLDENF
mORws 286 IVCWTPIHIVLIKALITI.....PETTFOTVSWHFCIALGYTNSCLNPVLYAFLDENF
ATla 250 FFSVVEHOLISTFDVLIOLGVHDCIKSDIVDTAMPITICTEYNNCLNPVLYAFLDENF
BK-2 280 IVCWTPIHIVLIKALITI.....PETTFOTVSWHFCIALGYTNSCLNPVLYAFLDENF

mORmouse 344 KRCFREFC...IPTSSSTIEQONSRIIRONTRHPSTANTVDRINHOLENLEAETAPLP
mORrat 344 KRCFREFC...IPTSSSTIEQONSRIIRONTRHPSTANTVDRINHOLENLEAETAPLP
mORbovin 347 KRCFREFC...IPTSSSTIEQONSRIIRONTRHPSTANTVDRINHOLENLEAETAPLP
mORhuman 346 KRCFREFC...IPTSSSTIEQONSRIIRONTRHPSTANTVDRINHOLENLEAETAPLP
mORpig 347 KRCFREFC...IPTSSSTIEQONSRIIRONTRHPSTANTVDRINHOLENLEAETAPLP
mORws 340 KRCFREFC...IPTSSSTIEQONSRIIRONTRHPSTANTVDRINHOLENLEAETAPLP
ATla 310 KRYFLOLLKYLPKAKSHS...SLSTKMSLSYRPSDNSSSAKIPASCFEVE---
BK-2 340 KAKSWVYOGVCKGGRSEPIOMENSMGTL...RTSTVEROIHKLODWACSRQ---

SEQ ID NO:

83
79
84
85
86
87
81
82

Figure 13